

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bander, Neil H.
- (ii) TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF  
PROSTATE CANCER
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
(B) STREET: Clinton Square, P.O. Box 1051  
(C) CITY: Rochester  
(D) STATE: New York  
(E) COUNTRY: U.S.A.  
(F) ZIP: 14603-1051
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 60/016,976  
(B) FILING DATE: 06-MAY-1996
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 06/022,125  
(B) FILING DATE: 18-JUL-1996
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Goldman, Michael L.  
(B) REGISTRATION NUMBER: 30,727  
(C) REFERENCE/DOCKET NUMBER: 19603/1172
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (716) 263-1304  
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60/016,976

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(1) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 391 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEO ID NO:1:

TCTCCTGTCA	GGAAGTGCAG	GTCTCCTCTC	TGAGGTCCAG	CTGCAACAGT	CTGGACCTGA	60
ACTGGTGAAG	CCTGGGACTT	CAGTGAGGAT	ATCCTGCAAG	ACTTCTGGAT	ACACATTCAC	120
TGAATATACC	ATACACTGGG	TGAAGCAGAG	CCATGGAAAG	AGCCTTGAGT	GGATTGGAAA	180
CATCAATCCT	AACAATGGTG	GTACCACCTA	CAATCAGAAG	TTCGAGGACA	AGGCCACATT	240
GA CTGTAGAC	AAGTCTCTCA	GTACAGCCTA	CATGGAGCTC	CGCAGCCTAA	CATCTGAGGA	300
TTCTGCAGTC	TATTATTGTG	CAGCTGGTTG	GAAC TTTGAC	TACTGGGGCC	AAGGCACCAC	360
TCTCAGAGTC	TCCTCAGCCA	AAACGACACC	C			391

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGTGTCGTT	TTGGCTGAGG	AGACTGTGAG	AGTGGTGCCT	TGGCCCCAGT	AGTCAAAGTT	60
CCAACCAGCT	GCACAATAAT	AGACTGCAGA	ATCCTCAGAT	GTTAGGCTGC	GGAGCTCCAT	120
GTAGGCTGTA	CTGGAGGACT	TGTCTACAGT	CAATGTGGCC	TTGTCCTCGA	ACTTCTGATT	180
GTAGGTGGTA	CCACCATTGT	TAGGATTGAT	GTTTCCAATC	CACTCAAGGC	TCTTTCCATG	240
GCTCTGCTTC	ACCCAGTGTA	TGGTATATTC	AGTGAATGTG	TATCCAGAAG	TCTTGCAGGA	300
TATCCTCACT	GAAGTCCCAG	GCTTCACCAG	TTCAGGTCCA	GACTGTTGCA	GCTGGACCTC	360
AGAGAGGACA	CCTGCAGTTC	CTAGCAGGAG	A			391

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 123 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Pro Val Arg Asn Cys Arg Cys Pro Leu Gly Pro Ala Ala Thr Val  
 1 5 10 15  
 Trp Thr Thr Gly Glu Ala Trp Asp Phe Ser Glu Asp Ile Leu Gln Asp  
 20 25 30  
 Phe Trp Ile His Ile His Ile Tyr His Thr Leu Gly Glu Ala Glu Pro  
 35 40 45  
 Trp Lys Glu Pro Val Asp Trp Lys His Gln Ser Gln Trp Trp Tyr His  
 50 55 60  
 Leu Gln Ser Glu Val Arg Gly Gln Gly His Ile Asp Cys Arg Gln Val  
 65 70 75 80  
 Leu Gln Tyr Ser Leu His Gly Ala Pro Gln Pro Asn Ile Gly Phe Cys  
 85 90 95  
 Ser Leu Leu Leu Cys Ser Trp Leu Glu Leu Leu Leu Gly Pro Arg His  
 100 105 110  
 His Ser His Ser Leu Leu Ser Gln Asn Asp Thr  
 115 120

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 130 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Leu Ser Gly Thr Ala Gly Val Leu Ser Glu Val Gln Leu Gln Gln  
 1 5 10 15  
 Ser Gly Pro Glu Leu Val Lys Pro Gly Thr Ser Val Arg Ile Ser Cys  
 20 25 30  
 Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr Thr Ile His Trp Val Lys  
 35 40 45

amb  
B11  
cat

[illegible]

(2) INFORMATION FOR ~~SEQ~~ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Leu 1	Ser	Cys	Gln 5	Glu	Leu	Gln	Val	Ser	Ser 10	Leu	Arg	Ser	Ser	Cys 15	Asn
Ser	Leu	Asp	Leu 20	Asn	Trp	Ser	Leu	Gly 25	Leu	Gln	Gly	Tyr	Pro 30	Ala	Arg
Leu	Leu	Asp 35	Thr	His	Ser	Leu	Asn 40	Ile	Pro	Tyr	Thr	Gly 45	Ser	Arg	Ala
Met	Glu 50	Arg	Ala	Leu	Ser	Gly 55	Leu	Glu	Thr	Ser	Ile 60	Leu	Thr	Met	Val
Val 65	Pro	Pro	Thr	Ile	Arg 70	Ser	Ser	Arg	Thr	Arg 75	Pro	His	Leu	Thr	Ser 80
Pro	Pro	Val	Gln	Pro 85	Thr	Trp	Ser	Ser	Ala 90	Ala	His	Leu	Arg	Ile 95	Leu
Gln	Ser	Ile	Ile 100	Val	Gln	Leu	Val	Gly 105	Thr	Leu	Thr	Thr	Gly 110	Ala	Lys
Ala	Pro	Leu 115	Ser	Gln	Pro	Ser	Gln 120	Pro	Lys	Arg	His	Pro 125			

*[Handwritten signature]*

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 345 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAGGTCCAGC TGCAACAGTC TGGACCTGAA CTGGTGAAGC CTGGGACTTC AGTGAGGATA 60  
TCCTGCAAGA CTTCTGGATA CACATTCACCT GAATATACCA TACACTGGGT GAAGCAGAGC 120  
CATGGAAAGA GCCTTGAGTG GATTGGAAAC ATCAATCCTA ACAATGGTGG TACCACCTAC 180  
AATCAGAAGT TCGAGGACAA GGCCACATTG ACTGTAGACA AGTCCTCCAG TACAGCCTAC 240  
ATGGAGCTCC GCAGCCTAAC ATCTGAGGAT TCTGCAGTCT ATTATTGTGC AGCTGGTTGG 300  
AACTTTGACT ACTGGGGCCA AGGCACCACT CTCACAGTCT CCTCA 345

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 345 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGAGGAGACT GTGAGAGTGG TGCCTTGGCC CCAGTAGTCA AAGTTCCAAC CAGCTGCACA 60  
ATAATAGACT GCAGAATCCT CAGATGTTAG GCTGCGGAGC TCCATGTAGG CTGTACTGGA 120  
GGACTTGTCT ACAGTCAATG TGGCCTTGTC CTCGAACTTC TGATTGTAGG TGGTACCACC 180  
ATTGTTAGGA TTGATGTTTC CAATCCACTC AAGGCTCTTT CCATGGCTCT GCTTCACCCA 240  
GTGTATGGTA TATTCAGTGA ATGTGTATCC AGAAGTCTTG CAGGATATCC TCACTGAAGT 300  
CCCAGGCTTC ACCAGTTCAG GTCCAGACTG TTGCAGCTGG ACCTC 345

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Thr  
 1 5 10 15  
 Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr  
 20 25 30  
 Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile  
 35 40 45  
 Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe  
 50 55 60  
 Glu Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
 65 70 75 80  
 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr  
 100 105 110  
 Val Ser Ser  
 115

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTATATGGAG CTGATGGGAA CATTGTAATG ACCCAATCTC CCAAATCCAT GTCCATGTCA 60  
 GTAGGAGAGA GGGTCACCTT GACCTGCAAG GCCAGTGAGA ATGTGGTTAC TTATGTTTCC 120  
 TGGTATCAAC AGAAACCAGA GCAGTCTCCT AACTGCTGA TATACGGGGC ATCCAACCGG 180  
 TACTGTTGGG TCCCGATCG CTTACAGGC AGTGGATCTG CAACAGATTT CACTCTGACC 240

ATCAGCAGTG TGCAGGCTGA AGACCTTGCA GATTATCACT GTGGACAGGG TTACAGCTAT 300  
CCGTACACGT TCGGAGGGGG GACCAAGCTG GAAATAAAAC GGGCTGATGC TGCACCAACT 360  
GTA 363

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 363 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TACAGTTGGT GCAGCATCAG CCCGTTTTAT TTCCAGCTTG GTCCCCCCTC CGAACGTGTA 60  
CGGATAGCTG TAACCCTGTC CACAGTGATA ATCTGCAAGG TCTTCAGCCT GCACACTGCT 120  
GATGGTCAGA GTGAAATCTG TTGCAGATCC ACTGCCTGTG AAGCGATCGG GGACCCCACT 180  
GTACCGGTTG GATGCCCCGT ATATCAGCAG TTTAGGAGAC TGCTCTGGTT TCTGTTGATA 240  
CCAGGAAACA TAAGTAACCA CATTCTCACT GGCCTTGCGA GTCAAGGTGA CCCTCTCTCC 300  
TACTGACATG GACATGGATT TGGGAGATTG GGTCATTACA ATGTTCCCAT CAGCTCCATA 360  
TAA 363

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 121 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Leu Tyr Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser  
1 5 10 15  
Met Ser Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys Lys Ala Ser  
20 25 30  
Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln  
35 40 45  
Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val  
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr  
65 70 75 80  
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln  
85 90 95  
Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile  
100 105 110  
Lys Arg Ala Asp Ala Ala Pro Thr Val  
115 120

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 114 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr Met Glu Leu Met Gly Thr Leu Pro Asn Leu Pro Asn Pro Cys Pro  
1 5 10 15  
Cys Gln Glu Arg Gly Ser Pro Pro Ala Arg Pro Val Arg Met Trp Leu  
20 25 30  
Leu Met Phe Pro Gly Ile Asn Arg Asn Gln Ser Ser Leu Leu Asn Cys  
35 40 45  
Tyr Thr Gly His Pro Thr Gly Thr Leu Gly Ser Pro Ile Ala Ser Gln  
50 55 60  
Ala Val Asp Leu Gln Gln Ile Ser Leu Pro Ser Ala Val Cys Arg Leu  
65 70 75 80  
Lys Thr Leu Gln Ile Ile Thr Val Asp Arg Val Thr Ala Ile Arg Thr  
85 90 95  
Arg Ser Glu Gly Gly Pro Ser Trp Lys Asn Gly Leu Met Leu His Gln  
100 105 110  
Leu Tyr

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile	Ile	Trp	Ser	Trp	Glu	His	Cys	Asn	Asp	Pro	Ile	Ser	Gln	Ile	His
1				5					10					15	
Val	His	Val	Ser	Arg	Arg	Glu	Gly	His	Leu	Asp	Leu	Gln	Gly	Gln	Glu
			20					25					30		
Cys	Gly	Tyr	Leu	Cys	Phe	Leu	Val	Ser	Thr	Glu	Thr	Arg	Ala	Val	Ser
		35					40					45			
Thr	Ala	Asp	Ile	Arg	Gly	Ile	Gln	Pro	Val	His	Trp	Gly	Pro	Arg	Ser
	50					55					60				
Leu	His	Arg	Gln	Trp	Ile	Cys	Asn	Arg	Phe	His	Ser	Asp	His	Gln	Gln
65					70					75				80	
Cys	Ala	Gly	Arg	Pro	Cys	Arg	Leu	Ser	Leu	Trp	Thr	Gly	Leu	Gln	Leu
				85					90					95	
Ser	Val	His	Val	Arg	Arg	Gly	Asp	Gln	Ala	Gly	Asn	Lys	Thr	Gly	Cys
			100					105					110		
Cys	Thr	Asn	Cys												
			115												

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 321 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AACATTGTAA TGACCCAATC TCCCAAATCC ATGTCCATGT CAGTAGGAGA GAGGGTCACC	60
TTGACCTGCA AGGCCAGTGA GAATGTGGTT ACTTATGTTT CCTGGTATCA ACAGAAACCA	120
GAGCAGTCTC CTAAACTGCT GATATACGGG GCATCCAACC GGTACACTGG GGTCCCCGAT	180
CGCTTCACAG GCAGTGGATC TGCAACAGAT TTCACTCTGA CCATCAGCAG TGTGCAGGCT	240
GAAGACCTTG CAGATTATCA CTGTGGACAG GGTTACAGCT ATCCGTACAC GTTCGGAGGG	300
GGGACCAAGC TGGAAATAAA A	321

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 321 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

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TTTTATTTCC AGCTTGGTCC CCCCTCCGAA CGTGTACGGA TAGCTGTAAC CCTGTCCACA      60
GTGATAATCT GCAAGGTCTT CAGCCTGCAC ACTGCTGATG GTCAGAGTGA AATCTGTTGC      120
AGATCCACTG CCTGTGAAGC GATCGGGGAC CCCAGTGTAC CGGTTGGATG CCCC GTATAT      180
CAGCAGTTTA GGAGACTGCT CTGGTTTCTG TTGATACCAG GAAACATAAG TAACCACATT      240
CTCACTGGCC TTGCAGGTCA AGGTGACCCT CTCTCCTACT GACATGGACA TGGATT TGGG      300
AGATTGGGTC ATTACAATGT T                                     321

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## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
1           5           10           15
Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr
20          25          30
Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile
35          40          45
Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50          55          60
Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala
65          70          75          80
Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr
85          90          95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100         105

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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 321 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACATTGTGA TGACCCAGTC TCACAAATTC ATGTCCACAT CAGTAGGAGA CAGGGTCAGC 60  
ATCATCTGTA AGGCCAGTCA AGATGTGGGT ACTGCTGTAG ACTGGTATCA ACAGAAACCA 120  
GGACAATCTC CTAAACTACT GATTTATTGG GCATCCACTC GGCACACTGG AGTCCCTGAT 180  
CGCTTCACAG GCAGTGGATC TGGGACAGAC TTCACTCTCA CCATTACTAA TGTTCAGTCT 240  
GAAGACTTGG CAGATTATTT CTGTCAGCAA TATAACAGCT ATCCTCTCAC GTTCGGTGCT 300  
GGGACCATGC TGGACCTGAA A 321

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 321 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTCAGGTCC AGCATGGTCC CAGCACCGAA CGTGAGAGGA TAGCTGTTAT ATTGCTGACA 60  
GAAATAATCT GCCAAGTCTT CAGACTGAAC ATTAGTAATG GTGAGAGTGA AGTCTGTCCC 120  
AGATCCACTG CCTGTGAAGC GATCAGGGAC TCCAGTGTGC CGAGTGGATG CCCAATAAAT 180  
CAGTAGTTTA GGAGATTGTC CTGGTTTCTG TTGATACCAG TCTACAGCAG TACCCACATC 240  
TTGACTGGCC TTACAGATGA TGCTGACCCT GTCTCCTACT GATGTGGACA TGAATTTGTG 300  
AGACTGGGTC ATCACAATGT C 321

0037090700

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly  
1 5 10 15  
Asp Arg Val Ser Ile Ile Cys Lys Ala Ser Gln Asp Val Gly Thr Ala  
20 25 30  
Val Asp Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile  
35 40 45  
Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly  
50 55 60  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser  
65 70 75 80  
Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Leu  
85 90 95  
Thr Phe Gly Ala Gly Thr Met Leu Asp Leu Lys  
100 105